

GenCore version 5.1.6
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OM protein - protein search, using swi model

Run on: June 25, 2003, 14:38:41 ; Search time 26.8605 Seconds

(without alignments)
843.812 million cell updates/sec

Title: US-09-622-613B-15

Sequence: 1 QNMATFOQKHINTPICT.....ICVKENQYPVHFAIGRCP 110

Scoring table: BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 10
Maximum DB seq length: 2000000000
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Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	08
1000	1000	1000

Maximum Match 100%

Listing first 45 summaries

Database

```

1:  sp:archaea:21:*
2:  sp:archaea:21:*
3:  sp:bacteria:21:*
4:  sp:fungi:21:*
5:  sp:inmetan:21:*
6:  sp:invertebrate:21:*
7:  sp:invertebrate:21:*
8:  sp:invertebrate:21:*
9:  sp:invertebrate:21:*
10: sp:invertebrate:21:*
11: sp:invertebrate:21:*
12: sp:invertebrate:21:*
13: sp:invertebrate:21:*
14: sp:invertebrate:21:*
15: sp:invertebrate:21:*
16: sp:invertebrate:21:*
17: sp:invertebrate:21:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to, the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	591.5	38.3	133	13	Q9PWR7	Q9PWR7 rana catestb
2	560.5	33.1	133	13	Q9BSM0	Q9BSM0 rana catestb
3	487.5	31.0	132	13	Q9BSM2	Q9BSM2 rana catestb
4	478.5	29.5	133	13	Q9BSL9	Q9BSL9 rana catestb
5	471.5	28.3	133	13	Q9BSL8	Q9BSL8 rana catestb
6	448.5	24.5	132	13	Q9BSM1	Q9BSM1 rana catestb
7	376	62.5	132	13	Q9DF78	Q9DF78 rana catestb
8	281.5	45.1	127	13	Q9SLV8	Q9SLV8 rana pipi
9	277.5	46.8	127	13	Q8U0V5	Q8U0V5 rana pipi
10	246	40.9	129	13	Q9DFY6	Q9DFY6 rana catestb
11	229.5	38.1	128	13	Q9DFY8	Q9DFY8 rana catestb
12	226.5	37.6	128	13	Q9DFY7	Q9DFY7 rana catestb
13	217.5	36.1	128	13	Q9DFY5	Q9DFY5 rana catestb
14	163	27.1	169	13	Q9W738	Q9W738 xenopus laae
15	131	21.8	170	6	Q9BEC1	Q9BEC1 traugulus ja
16	126	20.9	150	11	Q8V9D4	Q8V9D4 beryllmys bo

ALIGNMENTS

17	125.5	20.8	163	6	Q9BDC2	Q9BDC2	antilocapra
18	124.5	20.7	116	6	Q9TYC0	Q9TYC0	sus scrofa
19	124	20.6	150	11	Q8V8B8	Q8V8B8	rattus norv
20	122.5	20.3	144	6	Q9BH14	Q9BH14	antilocapra
21	120	19.9	150	11	Q8V9P2	Q8V9P2	rattus exul
22	116.5	19.4	152	11	Q8V8H9	Q8V8H9	rattus norv
23	115.5	19.2	119	6	Q9TVJ3	Q9TVJ3	bos taurus
24	114.5	19.0	124	6	Q95NE6	Q95NE6	bubalus bub
25	112.5	18.7	149	11	Q8VB95	Q8VB95	berylmys ba
26	112	18.6	134	6	Q9BDB9	Q9BDB9	tragulus ja
27	111.5	18.5	152	11	Q8VB04	Q8VB04	rattus tlor
28	111.5	18.5	156	6	Q8SQ05	Q8SQ05	leagotherix l
29	110.5	18.4	119	6	Q9TVJ0	Q9TVJ0	sagalinus oe
30	110.5	18.4	119	6	Q9TV28	Q9TV28	eulemur ful
31	110.5	18.4	124	6	Q9TFP2	Q9TFP2	bos taurus
32	109.5	18.2	142	6	Q9BEC3	Q9BEC3	tragulus ja
33	109.5	18.2	156	6	Q8SQ06	Q8SQ06	ateles geof
34	109	18.1	124	6	Q9BEC2	Q9BEC2	tragulus ja
35	108.5	18.0	156	6	Q8SQ08	Q8SQ08	saimiri sci
36	108.5	18.0	156	6	Q8SQ07	Q8SQ07	sagalinus oe
37	107.5	17.9	152	11	Q8V9P0	Q8V9P0	rattus fusc
38	106.5	17.7	116	6	Q9J9J3	Q9J9J3	phocoenoid
39	106.5	17.7	149	11	Q8VBD3	Q8VBD3	rattus exu
40	105.5	17.5	116	6	Q9J9J4	Q9J9J4	pseudorca c
41	105.5	17.5	119	6	Q9TSQ6	Q9TSQ6	cercopithec
42	104.5	17.4	119	6	Q9TVJ6	Q9TVJ6	gorilla gor
43	104.5	17.4	124	6	Q9YS40	Q9YS40	camelus bac
44	104	17.3	158	6	Q8SPY2	Q8SPY2	callithrix
45	103.5	17.2	158	6	Q8SPY3	Q8SPY3	sagalinus la

RESULT 1

ID	Q9PWR7	PRELIMINARY:	PRT:	133 AA.
AC	Q9PWR7			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Ribonuclease precursor.			
CN	RCR			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_Taxid=84400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=98156825; PubMed=9497370;			
RA	Huang H.C., Wang S.C., Lau Y.J., Lu S.C., Liao Y.D.;			
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RL	residues for RNase activity.";			
DR	J. Biol. Chem. 273:6395-6401(1998).			
DR	EMBL; AF039104; AADI0702.1; "			
DR	HSSP; P11916; 1BC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnaasea. 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	SIGNAL.			
FT	CHAIN	1	22	POTENTIAL.
FT	SEQUENCE	133 AA:	14762 MW:	RIBONUCLEASE.
				ATD62594FTDIEFQC CRC64;
Best Match	98.3%;	Score 591.5;	DB 13;	Length 133;
Best Local Similarity	99.1%;	Pred. No. 6,5e-61;		
Matches 110;	Conservative	0;	Mismatches	0;
			Indels	1;
				Gaps

Db 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 82
OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110
Db 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

RESULT 2

O98SMO

ID 098SMO PRELIMINARY: PRT: 133 AA.

AC 098SMO: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OS RNAse A-type ribonuclease rc208 precursor.
OC Rana catesbeiana (Bull frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNAse A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1;
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNAseA.
DR Pfam: PF00074; rnaasea; 1.
DR ProDom: PD000535; RNAseA; 1.
DR SMART: SM00092; RNAse_Pc; 1.
DR PROSITE: PS00127; RNAse_PANCREATIC; UNKNOWN_1.
KW Signal.

FT SIGNAL.
SQ SEQUENCE 133 AA: 14628 MW: 87FCF122C349E02 CRC64;
POTENTIAL.

Query Match 93.1%; Score 560.5; DB 13; Length 133;
Best Local Similarity 94.6%; Pred. No. 2, 6e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 59
Db 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 82
OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110
Db 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

RESULT 3

O98SM2

ID 098SM2 PRELIMINARY: PRT: 132 AA.

AC 098SM2: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
OS RNAse A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OC Rana catesbeiana (Bull frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNAse A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351210; AAK30256.1;
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNAseA.
DR Pfam: PF00074; rnaasea; 1.
DR ProDom: PD000535; RNAseA; 1.
DR SMART: SM00092; RNAse_Pc; 1.
DR PROSITE: PS00127; RNAse_PANCREATIC; UNKNOWN_1.
KW Signal.

FT SIGNAL.
SQ SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;
POTENTIAL.

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF351207; AAK30253.1;
DR EMBL: AF359578; AAL87036.1;
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNAseA.
DR Pfam: PF00074; rnaasea; 1.
DR ProDom: PD000535; RNAseA; 1.
DR SMART: SM00092; RNAse_Pc; 1.
DR PROSITE: PS00127; RNAse_PANCREATIC; UNKNOWN_1.
KW Signal.

FT CHAIN 23 132 RC-RNASE7.
SQ SEQUENCE 132 AA: 14412 MW: 131A745187978687 CRC64;
POTENTIAL.

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 59
Db 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 82
OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 109
Db 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 132

RESULT 4

O98SL9

ID 098SL9 PRELIMINARY: PRT: 133 AA.

AC 098SL9: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OS RNAse A-type ribonuclease rc212 precursor.
OC Rana catesbeiana (Bull frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNAse A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351210; AAK30256.1;
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNAseA.
DR Pfam: PF00074; rnaasea; 1.
DR ProDom: PD000535; RNAseA; 1.
DR SMART: SM00092; RNAse_Pc; 1.
DR PROSITE: PS00127; RNAse_PANCREATIC; UNKNOWN_1.
KW Signal.

FT SIGNAL.
SQ SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;
POTENTIAL.

Query Match 79.5%; Score 478.5; DB 13; Length 133;
Best Local Similarity 78.4%; Pred. No. 8, 4e-48;
Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 59
Db 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNFTFISSATTVKATCGVINMV 82
OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110
Db 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

RESULT 5

O98SL8

Oy		1 QNMATFOCKHILINPII-CNTIMDNNIYIVGGCGRVWTFLLISSATTYKAICTGY-NNM 59 .: : : : : : :	Matches 86; Conservative 7; Mismatches 16; Indels 1; Gaps 1;
Dd		23 QDMPTFOGKHIPSSSIDCNTIMDKDIYIVGCCRKAVTFLITSATTYKAICTGLSNV 82 : : : : : :	
Oy		60 LSTRPQUNTCRTSITPRCPYSSTRETNICYKCENOVVFHFAGIGRC 109 : : : : : :	
Dd		83 LSTRFOLXXTRFTITSRPCPYSSKETNKICVCENEYPVHFAGIGKC 132 : : : : : :	
RESULT 7			
ID	Q9DF78	PRELIMINARY: PRT: 132 AA.	
AC	Q9DF78:		
Dt	01-MAR-2001 (TREMBLrel. 16; Created)		
Dt	01-OCT-2001 (TREMBLrel. 18; Last sequence update)		
Dt	01-DEC-2001 (TREMBLrel. 19; Last annotation update)		
Dt	RC-RNASELI ribonuclease precursor.		
OS	Rana catesbeiana (bull frog).		
OC	Euryarchaea: Chordata: Craniata: Vertebrata: Euteleostomi: Amphibia: Metazoa: Chordata: Anura: Neobatrachia: Ranoidae: Ranae. NCBI_TaxID=8400;		
OX	[1]		
Rn	SEQUENCE FROM N.A.		
Rc	TISSEU=LIVER;		
Rx	MEDLINE=20512555; PubMed=11058105; Liao Y.-D., Huang H.-C., Liu Y.-J., Wei C.-W., Tang P.C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL AF288642; AAG30414.2; -		
Rf	HSSP; PI1916; IBC4.		
Rt	"InterPro: IPRO01427; RNaseA."		
Rt	Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";		
Rl	Nucleic Acids Res. 28:4097-4104(2000).		
Rn	[2]		
Rp	SEQUENCE FROM N.A.		
Rc	TISSEU=LIVER;		
Ra	Liao Y.-D., Huang H.-C., Liu Y.-J., Wei C.-W., Tang P.C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/Genbank/DDBJ databases. EMBL AF288642; AAG30414.2; -		
Rr	HSSP; PI1916; IBC4.		
Dr	Interpro: IPRO01427; RNaseA.		
DR	pfam: PF00074; rnasea: 1.		
DR	Prodrom: PD000535; RNaseA: 1.		
DR	SMART: SM00092; RNase_Pc: 1.		
Kw	PROSITE: PS00127; RNASE-PANCREATIC; UNKNOWN_1.		
km	Signal.		
Ft	SIGNAL.		
Ft	CHAIN		
SO	SEQUENCE 132 AA: 14625 MW; DDD9AS1745ZEBE5 CGC64;		
	Query Match	62.5%; Score 376; DB 13; Length 132:	
	Best Local Similarity	65.8%; Pred.No. 6.4e-36;	
	Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;		
Oy		1 QNMATFOCKHILINPII-CNTIMDNNIYIVGGCGRVWTFLLISSATTYKAICTGY-NNM 58 : : : : : :	
Dd		22 QNMAREKRKHHTSPSSIDCNTIMAKAIYVGKKERTFFLSSEDNVKALCSGVSDPK 81 : : : : : :	
Oy		59 VLUSTRPQUNTCRTSITPRCPYSSTRETNYVICVKENOVPVHFAGIGRC 109 : : : : : :	
Dd		82 ELSTTSFKLNLCIRDSTITRPPCFPHPSPDNNKIYCCKEKQLPVHFGIGKC 132 : : : : : :	
RESULT 8			
ID	G918V8	PRELIMINARY: PRT: 127 AA.	
AC	G918V8:		
Dt	01-OCT-2000 (TREMBLrel. 15; Created)		
Dt	01-OCT-2000 (TREMBLrel. 15; Last sequence update)		
Dt	01-DEC-2001 (TREMBLrel. 19; Last annotation update)		
DE	Oncogene variant rapIR precursor.		
OS	Rana pipiens (Northern leopard frog).		
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrate: Euteleostomi; Amplbia: Batrachia: Anura: Neobatracchia: Ranoidae: Rana. NCBI_TaxID=8404;		
OX	[2]		

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF159166; AAD41901.1; -
 DR HSSP; P00656; IL5Q.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 SO SEQUENCE 169 AA; 18891 MW; D969FE43B3CE1B8 CRC64;

Query Match 27.1%; Score 163; DB 13; Length 169;
 Best Local Similarity 39.3%; Pred. No. 4.3e-11;
 Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

OY 1 QNNATFOOKHII--NTPICN-TIMDNIIYVGCGCKRVNTEFI-ISSATVKAICTGVIN 56
 DB 28 QNINAFMEKHIVGEGACTNCNOTIKDKNIRF-KNCKCFRNTFIHDTNGKKVKEKAGIYK 86
 OY 57 MN-VLSTTRFQNLNCTRTSITPRP--CPYSSRTETNYICVKNQYVPHFAG 105
 DB 87 STVVISKELLPLTDCLMGRTARPPNCAYNQTRTGVINITCENNYPVHFG 138

RESULT 15

O9BEC1 PRELIMINARY; PRT; 170 AA.
 AC O9BEC1;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Brain-type ribonuclease ribonuclease precursor (Fragment).
 GN RNase B.
 OS Tragus javanicus (lesser Malay chevrolain).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
 OC Tragulidae; Tragulus.
 OC NCB1_TaxID-9849;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21347458; PubMed-11453981;
 RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
 RA Wamelis H.W., Belantema J.J.;
 RT "Secretory ribonucleases in the primitive ruminant chevrolain
 (Tragus javanicus).";
 RT Eur. J. Biochem. 268:3890-3897(2001).
 CC 1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR EMBL: AJ271299; CAC24723.1; -
 DR HSSP; P00656; IL5Q.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Endonuclease; Hydrolase; Nuclease; Signal.
 FT NON_TER 1
 FT SIGNAL <1 19
 FT CHAIN 20 170 POTENTIAL.
 SO SEQUENCE 170 AA; 18832 MW; ABCCE7E1E5549AA0 CRC64;
 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.

Query Match 21.8%; Score 131; DB 6; Length 170;
 Best Local Similarity 33.1%; Pred. No. 2.2e-07;
 Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

OY 4 ATFOOKHII-----INTPIICNTIMDNIIYVGCGCKRVNTEFIISATVKAICT-----52
 DB 25 AKFRROHLDAGNSSINSN-YCNLMKRR-KWTHGRCKPVNTEFIHESLEDKAICSEKNIT 82
 OY 53 ---GVIMNVLSTTRFQNLNCTRTSITPRP--CPYSSRTETNYICVKNQYVPHFAGI 106
 DB 83 CKNGOPNCHOSNST-AMITDCROTGSGSKYPNCAVKTOKOKYIIVACEGTPSPVPHFDGS 141
 OY 107 GRCP 110

DB 142 AVLP 145

Search completed: June 25, 2003, 14:55:18
 Job time : 26.9438 secs